RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/535,458
Source: IFW0
Date Processed by STIC: 7/5/06

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IFWO

RAW SEQUENCE LISTING DATE: 07/05/2006
PATENT APPLICATION: **US/10/535,458** TIME: 08:51:01

Input Set : **N:\SSLM\10535458.txt**
Output Set: **N:\CRF4\07052006\J535458.raw**

3 <110> APPLICANT: McLachlan, Karen
4 Gately, Dennis
6 <120> TITLE OF INVENTION: NOVEL GENE TARGETS AND LIGANDS THAT BIND THERETO FOR TREATMENT AND
7 DIAGNOSIS OF COLON CARCINOMAS
9 <130> FILE REFERENCE: 2159.0640005/EKS/J-H
C--> 11 <140> **CURRENT APPLICATION NUMBER: US/10/535,458**
C--> 12 <141> **CURRENT FILING DATE: 2005-05-19**
14 <150> PRIOR APPLICATION NUMBER: US 60/427,564
15 <151> PRIOR FILING DATE: 2002-11-20
17 <160> NUMBER OF SEQ ID NOS: 73
19 <170> SOFTWARE: PatentIn version 3.1
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22 <211> LENGTH: 149
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
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35 <211> LENGTH: 679
36 <212> TYPE: DNA
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44 gaaatgttga tttaggaggt attgccttcg agaagataaa ggaggagaag aggagagcat 180
46 catgcaagct agagaagaga aagaagaaaa gtattctggg gaatgtctcc tttgggagca 240
48 gaaagaagac tctgacggag cagccatcca ggaagtggaa tgagatccag gagaggaagg 300
50 agtttcagaa ggcaggagct ggtcctctat gtcatgaaat gtagagggtg aggccaagga 360
52 ggacctgaga gaaggtaatt agatttggtg tttacaggct ggtccctgtg gccagccacc 420
54 ccacccactt taaaatattt actctacaaa tgttaatgtg tgaagagttg catgccagaa 480
56 tatttatggc atcagtgttg gtggatacag aacattggga aacaacccat taatagcaga 540
58 atggtaaatc tggccagtga atagtatagc tttttaaaag gaggctgatg tctgaattca 600
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88 aaagaaaact tcaacactgt ggagcacatt gaggaggtgg cctataatgc actgtccttt 180
90 gtgtggaacg tgaatgaaga ggccaaggtg ttcatcggcg taaactgtct gagcacagac 240
92 ttttcctcac aaaagggggt gaagggtgtc cccctgaacc tgcagattga cacctatgac 300
94 tgtggcttgg gcactgagcg cctggtacac cgtgctgtct gccagatcaa gatcttctgt 360
96 gacaagggag ctgagaggaa gatgcgcgat gacgagcgga agcagttccg gaggaaggtc 420
98 aagtgccctg actccagcaa cagtggcgtc aagggctgcc tgctgtcggg cttcaggggc 480
100 aatgagacga cctaccttcg gccagagact gacctggaga cgccacccgt gctgttcatc 540
102 cccaatgtgc acttctccag cctgcagcgg tctggagggg cagccccctc ggcaggaccc 600
104 agcagctcca acaggctgcc tctgaagcgt acctgctcgc ccttcactga ggagtttgag 660
106 cctctgccct ccaagcaggc caaggaaggc gaccttcaga gagttctgct gtatgtgcgg 720
108 agggagactg aggaggtgtt tgacgcgctc atgttgaaga ccccagacct gaaggggctg 780
110 aggaatgcga tctctgagaa gtatgggttc cctgaagaga acatttacaa agtctacaag 840
112 aaatgcaagc gaggaatctt agtcaacatg gacaacaaca tcattcagca ttacagcaac 900
114 cacgtcgcct tcctgctgga catgggggag ctggacggca aaattcagat catccttaag 960
116 gagctgtaag gcctctcgag catccaaacc ctcacgacct gcaaggggcc agcagggacg 1020
118 tggccccacg ccacacacaa cctctccaca tgcctcagcg ctgttacttg aatgccttcc 1080
120 ctgagggaag aggcccttga gtcacagacc cacagacgtc agggccaggg agagacctag 1140
122 ggggtcccct ggcctggatc cccatggtat gcttgaatct gctccctgaa cttcctgcca 1200
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130 cttcaacttc agacaaagga tttctcaacc tttggtcagt taacttgaaa actcttgatt 1440
132 ttcagtgcaa atgactttta aaagacacta tattggagtc tctttctcag acttcctcag 1500
134 cgcaggatgt aaatagcact aacgatcgac tggaacaaag tgaccgctgt gtaaaactac 1560
136 tgccttgcca ctcactgttg tatacatttc ttatttacga ttttcatttg ttatatatat 1620
138 atataaatat actgtatata tatgcaacat tttatatttt tcatggatat gtttttatca 1680
140 tttcaaaaaa tgtgtatttc acatttcttg gacttttttt agctgttatt cagtgatgca 1740
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156 Leu Arg Phe Trp Lys His Trp His Ser Arg Gln Pro Thr Ala Lys Gln
157 20 25 30
160 Arg Val Ile Asp Val Ala Asp Cys Lys Glu Asn Phe Asn Thr Val Glu
161 35 40 45
164 His Ile Glu Glu Val Ala Tyr Asn Ala Leu Ser Phe Val Trp Asn Val
165 50 55 60

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168 Asn Glu Glu Ala Lys Val Phe Ile Gly Val Asn Cys Leu Ser Thr Asp
169 65                  70                  75                  80
172 Phe Ser Ser Gln Lys Gly Val Lys Gly Val Pro Leu Asn Leu Gln Ile
173                 85                  90                  95
176 Asp Thr Tyr Asp Cys Gly Leu Gly Thr Glu Arg Leu Val His Arg Ala
177             100                 105                 110
180 Val Cys Gln Ile Lys Ile Phe Cys Asp Lys Gly Ala Glu Arg Lys Met
181         115                 120                 125
184 Arg Asp Asp Glu Arg Lys Gln Phe Arg Arg Lys Val Lys Cys Pro Asp
185     130                 135                 140
188 Ser Ser Asn Ser Gly Val Lys Gly Cys Leu Leu Ser Gly Phe Arg Gly
189 145                 150                 155                 160
192 Asn Glu Thr Thr Tyr Leu Arg Pro Glu Thr Asp Leu Glu Thr Pro Pro
193                 165                 170                 175
196 Val Leu Phe Ile Pro Asn Val His Phe Ser Ser Leu Gln Arg Ser Gly
197             180                 185                 190
200 Gly Ala Ala Pro Ser Ala Gly Pro Ser Ser Ser Asn Arg Leu Pro Leu
201         195                 200                 205
204 Lys Arg Thr Cys Ser Pro Phe Thr Glu Glu Phe Glu Pro Leu Pro Ser
205     210                 215                 220
208 Lys Gln Ala Lys Glu Gly Asp Leu Gln Arg Val Leu Leu Tyr Val Arg
209 225                 230                 235                 240
212 Arg Glu Thr Glu Glu Val Phe Asp Ala Leu Met Leu Lys Thr Pro Asp
213                 245                 250                 255
216 Leu Lys Gly Leu Arg Asn Ala Ile Ser Glu Lys Tyr Gly Phe Pro Glu
217             260                 265                 270
220 Glu Asn Ile Tyr Lys Val Tyr Lys Lys Cys Lys Arg Gly Ile Leu Val
221         275                 280                 285
224 Asn Met Asp Asn Asn Ile Ile Gln His Tyr Ser Asn His Val Ala Phe
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229 305                 310                 315                 320
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241 <400> SEQUENCE: 6
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246 tacaggatca ctgtgggacg gtggggctgg ccacctgggc aggccactta cccagcggcc    180
248 ccctctgtct ccaggtgttc atcggcgtaa actgtctgag cacagacttt tcctcacaaa    240
250 agggggtgaa gggtgtcccc ctgaacctgc agattgacac ctatgactgt ggcttgggca    300
252 ctgagcgcct ggtacaccgt gctgtctgcc agatcaagat cttctgtgac aagggagctg    360
254 agaggaagat gcgcgatgac gagcggaagc agttccggag gaaggtcaag tgccctgact    420
256 ccagcaacag tggcgtcaag ggctgcctgc tgtcgggctt caggggcaat gagacgacct    480
258 accttcggcc agagactgac ctggagacgc cacccgtgct gttcatcccc aatgtgcact    540
260 tctccagcct gcagcggtct ggaggggcag ccccctcggc aggacccagc agctccaaca    600
262 ggctgcctct gaagcgtacc tgctcgccct tcactgagga gtttgagcct ctgccctcca    660
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264 agcaggccaa ggaaggcgac cttcagagag ttctgctgta tgtgcggagg gagactgagg    720
266 aggtgtttga cgcgctcatg ttgaagaccc cagacctgaa ggggctgagg aatgcgatct    780
268 ctgagaagta tgggttccct gaagagaaca tttacaaagt ctacaagaaa tgcaagcgag    840
270 gaatcttagt caacatggac aacaacatca ttcagcatta cagcaaccac gtcgccttcc    900
272 tgctggacat gggggagctg gacggcaaaa ttcagatcat ccttaaggag ctgtaaggcc    960
274 tctcgagcat ccaaaccctc acgacctgca aggggccagc agggacgtgg ccccacgcca   1020
276 cacacaacct ctccacatgc ctcagcgctg ttacttgaat gccttccctg agggaagagg   1080
278 cccttgagtc acagacccac agacgtcagg gccagggaga gacctagggg gtcccctggc   1140
280 ctggatcccc atggtatgct tgaatctgct ccctgaactt cctgccagtg cctccccgta   1200
282 ccccaaaaca atgtcaccat ggttaccacc tacccagaag actgttccct cctcccaaga   1260
284 cccttgtctg cagtggtgct cctgcaggct gcccgttaag atggtggcgg cacacgctcc   1320
286 ctcccgcagc accacgccag ctggtgcggc ccccactctc tgtcttcctt caacttcaga   1380
288 caaaggattt ctcaaccttt ggtcagttaa cttgaaaact cttgattttc agtgcaaatg   1440
290 acttttaaaa gacactatat tggagtctct ttctcagact tcctcagcgc aggatgtaaa   1500
292 tagcactaac gatcgactgg aacaaagtga ccgctgtgta aaactactgc cttgccactc   1560
294 actgttgtat acatttctta tttacgattt tcatttgtta tatatatata taaatatact   1620
296 gtatatatat gcaacatttt atatttttca tggatatgtt tttatcattt caaaaaatgt   1680
298 gtatttcaca tttcttggac ttttttttagc tgttattcag tgatgcattt tgtatactca   1740
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304 <211> LENGTH: 195
305 <212> TYPE: PRT
306 <213> ORGANISM: Homo sapiens
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318 Gly Asn Glu Thr Thr Tyr Leu Arg Pro Glu Thr Asp Leu Glu Thr Pro
319         35                  40                  45
322 Pro Val Leu Phe Ile Pro Asn Val His Phe Ser Ser Leu Gln Arg Ser
323     50                  55                  60
326 Gly Gly Ala Ala Pro Ser Ala Gly Pro Ser Ser Ser Asn Arg Leu Pro
327 65                  70                  75                  80
330 Leu Lys Arg Thr Cys Ser Pro Phe Thr Glu Glu Phe Glu Pro Leu Pro
331                 85                  90                  95
334 Ser Lys Gln Ala Lys Glu Gly Asp Leu Gln Arg Val Leu Leu Tyr Val
335             100                 105                 110
338 Arg Arg Glu Thr Glu Glu Val Phe Asp Ala Leu Met Leu Lys Thr Pro
339         115                 120                 125
342 Asp Leu Lys Gly Leu Arg Asn Ala Ile Ser Glu Lys Tyr Gly Phe Pro
343     130                 135                 140
346 Glu Glu Asn Ile Tyr Lys Val Tyr Lys Lys Cys Lys Arg Gly Ile Leu
347 145                 150                 155                 160
350 Val Asn Met Asp Asn Asn Ile Ile Gln His Tyr Ser Asn His Val Ala
351                 165                 170                 175
354 Phe Leu Leu Asp Met Gly Glu Leu Asp Gly Lys Ile Gln Ile Ile Leu
355             180                 185                 190
358 Lys Glu Leu
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Input Set : N:\SSLM\10535458.txt
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364 <212> TYPE: DNA
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372 gccatgatga gagtcaatgg agatgatgag agtgttgcgg ccttgagctt cctctatgat 180
374 tactacatgt cgatgctctt cccagatatc ctgaaaacct ccccggaacc cccatgtcca 240
376 gaggactacc ccagcctcaa aagtgacttt gaatacaccc tgggctcccc caaagccatc 300
378 cacatcaagt caggcgagtc acccatggcc tacctcaaca aaggccagtt ctaccccgtc 360
380 accctgcgga ccccagcagg tggcaaaggc cttgccttgt cctccaacaa agtcaagagt 420
382 gtggtgatgg ttgtcttcga caatgagaag gtcccagtag agcagctgcg cttctggaag 480
384 cactggcatt cccggcaacc cactgccaag cagcgggtca ttgacgtggc tgactgcaaa 540
386 gaaaacttca acactgtgga gcacattgag gaggtggcct ataatgcact gtcctttgtg 600
388 tggaacgtga atgaagaggc caaggtgttc atcggcgtaa actgtctgag cacagacttt 660
390 tcctcacaaa agggggtgaa gggtgtcccc ctgaacctgc agattgacac ctatgactgt 720
392 ggcttgggca ctgagcgcct ggtacaccgt gctgtctgcc agatcaagat cttctgtgac 780
394 aagggagctg agaggaagat gcgcgatgac gagcggaagc agttccggag gaaggtcaag 840
396 tgccctgact ccagcaacag tggcgtcaag ggctgcctgc tgtcgggctt caggggcaat 900
398 gagacgacct accttcggcc agagactgac ctggagacgc cacccgtgct gttcatcccc 960
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402 ctcattttcc tgcgtgtgat ggaaaatgtc tttttcactt cattgcaggc agccccctcg 1080
404 gcaggaccca gcagctccaa caggctgcct ctgaagcgta cctgctcgcc cttcactgag 1140
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408 tatgtgcgga gggagactga ggaggtgttt gacgcgctca tgttgaagac cccagacctg 1260
410 aaggggctga ggaatgcgat ctctgagaag tatgggttcc ctgaagagaa catttacaaa 1320
412 gtctacaaga aatgcaagcg aggaatctta gtcaacatgg acaacaacat cattcagcat 1380
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420 <211> LENGTH: 485
421 <212> TYPE: PRT
422 <213> ORGANISM: Homo sapiens
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434 Asn Pro Leu Thr Ala Ala Thr Lys Ala Met Met Arg Val Asn Gly Asp
435 35 40 45
438 Asp Glu Ser Val Ala Ala Leu Ser Phe Leu Tyr Asp Tyr Tyr Met Ser
439 50 55 60
442 Met Leu Phe Pro Asp Ile Leu Lys Thr Ser Pro Glu Pro Pro Cys Pro
443 65 70 75 80
446 Glu Asp Tyr Pro Ser Leu Lys Ser Asp Phe Glu Tyr Thr Leu Gly Ser
447 85 90 95
450 Pro Lys Ala Ile His Ile Lys Ser Gly Glu Ser Pro Met Ala Tyr Leu

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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:18; N Pos. 16,93
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Seq#:20; N Pos. 434,1171,1212,1220,1224
Seq#:22; N Pos. 3,8,703,744,754,759,777,784,805,824,831,850,861,864,875,879
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Seq#:22; N Pos. 1142,1145,1151,1159,1163,1168,1176,1190
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Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:56,57,58,59,60,61,62,63,64,65,73

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Input Set : **N:\SSLM\10535458.txt**
Output Set: **N:\CRF4\07052006\J535458.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1075 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:60
M:341 Repeated in SeqNo=17
L:1104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
M:341 Repeated in SeqNo=18
L:1166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
M:341 Repeated in SeqNo=20
L:1240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
M:341 Repeated in SeqNo=22
L:1295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
M:341 Repeated in SeqNo=23
L:1709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
M:341 Repeated in SeqNo=27
L:1764 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
M:341 Repeated in SeqNo=28
L:1819 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
M:341 Repeated in SeqNo=29
L:1870 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
M:341 Repeated in SeqNo=30
L:2658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:240
M:341 Repeated in SeqNo=36
L:3079 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:120
M:341 Repeated in SeqNo=41
L:3448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0
M:341 Repeated in SeqNo=46
L:3500 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:0
M:341 Repeated in SeqNo=48